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(b) calculating for each polynucleotide from the first and second values a position, and from the third value a peak at that position in a multi-dimensional display space; and

(c) displaying the peak for each polynucleotide at the calculated position for the polynucleotide in the display, the resulting display representing thereby a molecular topography of gene expression,

wherein ordered values of the first and second characteristics are arranged upon first and second ordinates that define a plane in the multi-dimensional display space, the values of the first and second characteristics for each polynucleotide is displayed define a position in the plane, and the peak calculated for each polynucleotide displayed in another dimension of the multi-dimensional display space at the defined position for that polynucleotide in the plane.

10. (Amended) The method of claim 9, wherein the 3'-end fragments are generated by [READS] Restriction Enzyme Analysis of Differentially Expressed Sequences (READS).

24. (Amended) A computer program product, usable in a computer system, for analyzing and displaying gene expression in a molecular topography, the computer program product comprising:

a first program code that generates a gene expression profile of a plurality of gene-expression indicating polynucleotides including for each of the polynucleotides:

(i) a first value for a first polynucleotide characteristic,

(ii) a second value for a second polynucleotide- characteristic different from said first characteristic, and

(iii) a third value that is a measure of the quantity of the polynucleotide;

a second program code that calculates for each polynucleotide from the first and second values a position, and from the third value a peak at that position in a multi-dimensional display space; and

a third program code that displays the peak for each polynucleotide at the calculated position for the polynucleotide in a display, the resulting display representing thereby a molecular topography of gene expression,

wherein ordered values of the first and second characteristics are arranged upon first and second ordinates that define a plane in the multi-dimensional display space, the values of the first and second characteristics for each polynucleotide displayed define a position in the plane, and the peak calculated for each polynucleotide is displayed in another dimension of the multi-dimensional display space at the defined position for that polynucleotide in the plane.